In the Specification:

Please replace the third full paragraph on page 19 with the following paragraph:

Techniques for eliciting the differentiation of HS cells of the present invention into follicular cells, as well as epidermal cells are also contemplated. For example, Taylor et al., Cell, **102**: 451-361 (2000), incorporated by reference herein, describe ES cell-derived follicle and epidermis cells may be used for hair replacement and skin graft therapies. These techniques can be adapted for use with the HS cells of the present invention. The expression of particular regulatory genes may also be used to direct differentiation. See, for example, Hole et al., Blood, ~~90~~ 88(4):1266-1276 (1996~~a~~), and Hole et al., Bailliere's ~~Battieres.~~ Clin. ~~Hematol.~~ Haematol., **10**(3):467-483 ~~3:467-483~~ (1997), incorporated by reference herein, relating to hematopoietic genes. Likewise, preliminary evidence suggests that nuclear regulatory factors involved in lipid metabolism, including but not limited to PPARs (PPARδ and PPARγ) and C/EBPδ (C/EBPβ, C/EBPδ and C/EBPα), may also be triggers of terminal differentiation of preadipocytes into adipocytes. Such factors would find utility in the context of the differentiation methods of the present invention.

Please replace the last paragraph on page 41 with the following paragraph:

For ES cells, apparent differences in outcome of hematopoietic differentiation may be due to several different approaches by these groups. Some have used exogenous cytokines, which may amplify otherwise low levels of specific lineage commitment. Indeed, it is clear that the differentiating ES cells themselves contain transcripts for a wide range of hematopoietic cytokines (Hole et al., Blood, ~~90~~88(4):1266-1267 (1996~~a~~); Hole et ~~al.~~ al. Gene Technology, Berlin, Springer, pp 3-10 (1996~~b~~)) and factors (Keller et al., Mol. Cell. Biol., **13**:473-486 (1993~~b~~)), which can influence the commitment process.

Please replace the first paragraph on page 42 with the following paragraph:

Lymphoid progenitors can be produced and isolated following HS cell differentiation *in vitro*. Adoptive transfer into mice whose lymphoid compartment is compromised by genetic lesion results in ES cell-derived lymphoid repopulation over both the long and short term (Potocnik et al., Immunol. Lett., **57**:131-137 (1997)). Early reports suggest that repopulating ability of ES cell-derived hematopoietic progenitors maybe restricted to the lymphoid system, however, further studies show that ES cell-derived cells can demonstrate long-term, multilineage, hematopoietic repopulating potential (Palacios et al., Proc. Natl. Acad. Sci. USA, **92**:7530-7534 (1995); Hole et al., Blood, ~~90~~**88(4)**:1266-1276, (1996~~a~~)).

Please replace the second paragraph on page 42 with the following paragraph:

Long-term repopulating hematopoietic stem cells can be identified following differentiation of ES cells *in vitro*. By characterizing the time course of this differentiation, ES cells can be used to examine the differential expression of genes at the stage at which hematopoietic stem cells are first emerging as distinct cell type. Hematopoietic stem cells are present within a comparatively brief period of differentiation; multilineage repopulating activity is present at day 4 of differentiation, but not found either at day 3 or day 5. (Hole et al., Blood, ~~90~~**88(4)**:1266-1276, (1996~~a~~)). Expression of known hematopoietic genes reinforces the importance of this period in hematopoietic differentiation; expression is dramatically up-regulated in this period (Hole et al., Blood, ~~90~~**88(4)**:1266-1276, (1996~~a~~); Hole and Graham, Bailliere's ~~Battieres~~ Clin. ~~Hematol.~~ Haematol., **3**:467-483 (1997)). Using a subtractive hybridization approach, Hole and Graham, ~~*Battieres*~~ *Bailliere's Clin.* ~~*Hematol.*~~ *Haematol.*, **3**:467-483 (1997) demonstrated that this model of *in vitro* differentiation is a rich source of hematopoietic genes; at least two of the novel genes identified are expressed in embryogenesis and hematopoietic cell lines in a manner consistent with early hematopoietic commitment.

Please replace the paragraph beginning at the bottom of page 72 with the following paragraph:

After 3 days, the medium is replaced with LIF-free stem cell medium containing 20ng/ml hepatic growth factor (Sigma, H-1404) for 6 days, and then in LIF-free stem cell medium containing 10ng/ml OSM (Sigma, O-9635), 10 μM Dexamethasone (Sigma, D-6645), 5 μg/ml selenious acid (Aldrich, 22985-7), 50 μg/ml insulin (Invitrogen, I-1882), and 50 μg/ml transferrin (Sigma, T-2036). The differentiated cells are then analyzed for hepatic specific gene expression. The genes analyzed, the annealing temperature for PCR, expected product ~~seizes~~ sizes, and the primer sequences in RTPCR are as follows: transthyretin (TTR), 55°C, 225 bp, 5-CTC ACC ACA GAT GAG AAG (SEQ ID NO:1), 5-GGC TGA GTC TCT CAA TTC (SEQ ID NO:2); α-fetoprotein (AFP), 55°C, 173 bp, 5-TCG TAT TCC AAC AGG AGG (SEQ ID NO:3), 5-AGG CTT TTG CTT CAC CAG (SEQ ID NO:4); α-1-anti-trypsin (AAT), 55°C, 484 bp, 5-AAT GGA AGA AGC CAT TCG AT (SEQ ID NO:5), 5-AAG ACT GTA GCT GCT GCA GC (SEQ ID NO:6); Albumin (ALB), 55°C, 260 bp, 5-GCT ACG GCA CAG TGC TTG (SEQ ID NO:7), 5-CAG GAT TGC AGA CAG ATA GTC (SEQ ID NO:8); glucose-6-phosphatase (G6P), 55°C, 210 bp, 5-CAG GAC TGG TTC ATC CTT (SEQ ID NO:9), 5-GTT GCT GTA GTA GTC GGT (SEQ ID NO:10); tyrosine ~~aminotrnasferase~~ aminotransferase (TAT), 50°C, 206 bp, 5-ACC TTC AAT CCC ATC CGA (SEQ ID NO:11), 5-TCC CGA CTG GAT AGG GTA G (SEQ ID NO:12); β-actin, 55°C, 200 bp, 5-TTC CTT CTT GGG TAT GGA AT (SEQ ID NO:13), 5-GAG CAA TGA TCT TGA TCT TC (SEQ ID NO:14); and SEK1, 50°C, 300 bp, 5-TGT ATG GAG CTC ATG TCT ACC (SEQ ID NO:15)~~;~~, 5-GTC TAT TCT TTC AGG TGC CA (SEQ ID NO:16).